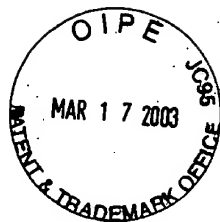


#31



- 51 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: GRIFFITHS, RICHARD
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F13

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- (B) STREET: 4 Upway Road
- (C) CITY: Oxford
- (E) COUNTRY: United Kingdom
- (F) POSTAL CODE (ZIP): OX3 9QH

(ii) TITLE OF INVENTION: AVIAN GHD GENES AND THEIR USE IN METHODS FOR
SEX IDENTIFICATION IN BIRDS

(iii) NUMBER OF SEQUENCES: 39

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO PCT/GB96/01341

(B) FILING DATE: 05-JUN-1996

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9511439.3

(B) FILING DATE: 06-JUN-1995

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Warren M Cheek, Jr.

(B) REGISTRATION NUMBER: 33,367

(C) REFERENCE/DOCKET NUMBER: 263/PPNTIR1172US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202)-721-8200

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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 723 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCCGGTCGGA GGTTC AAGG AATGACTAGA TGTGGCACTT AGTGCCATGG TCTAGTTGAC	60
AAGGTGATGG TTGGTCAAAA GTTGGACTCG ATGATCTCAG AGTTTTTTTTC CAGCCTTAAT	120
AATTCTATGA ATTCTGTAAT TTTATTCTTG ATCTTTTTTGA GCGAAGTTTG TTTGGGGATT	180
TTAGTTTGGT TTCCCTGTCA CTGTTTTTCTT TCCTTGAAAC TGACTTTCAT TTGCAACATG	240
AGAATTGCTG TATTTGTCAG GTTACAAGTA GTGCAATGGC TGCTTAGAAG TAGTGAGAAA	300
CATTTAGGGA AATACTGGAG TGAAGCAAAC ACAGTGGTAC TGCCAAACTG TAGCTTTGGG	360
ATTTGAGGAG CCACAGAGTT GTATATAAAT TTGTTTAATG ATATCCTGCC CCTGCCTTCC	420
ATTAATTGCT TGTTTTATGA AACCACTCTT TTTTTTTTTT TTTTTTTTTT GGCTTCTTCA	480
TATCCTGTGG TAATGAGTTA ATGCATTTAG AAGCACATGG CAGAACTAGG AGATCTGTGG	540
ATGACAGTGG TACAGGAGCT CTGAATTTTT TAGATAAACT ATGAGAGTGG AAACAGAAAT	600
CTGAGGCTAG TTTCTTGAGC TGAAGTAAA TTTGTGAGA ATATTTTCAA GACTACATTA	660
GTTGTGTGTT TGAGGAAAAA TAAAATGTTT AAGTTGTCCA TTCCTGAAA CCTCCCGACC	720
GGG	723

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATTCTTCCAG ATGATCCTGA TAAAAAACCA CAAGCAAAAC AGTTACAGAC CAAAAAACCA	60
CAAGCAAAAC AGTTACAGAC CCGTGCAGAC TACCTCATCA AACTACTTAG CAGAGATCTT	120
GCAAAAAGAG AGGCTCAGAG ACTTTGTGGT GCG	153

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATTTTACCTG ATGATCCAGA CAAGAAACCC CAGGCAAAGC AGCTACAGAC CAAGAAACCC	60
CAGGCAAAGC AGCTACAGAC CCGTGCAGAC TACCTCATTA AATTACTGAA TAAAGACCTT	120
GCAAGAAAGG AAGCACAAAG GCTTGCTGGT GCA	153

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATTTTACCTG ATGATCCAGA TAAGAAACCC CAGGCTAAGC AGTTACAGAC CAAGAAACCC	60
CAGGCTAAGC AGTTACAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT	120
GCAAGAAAGG AAGCACAGAG ACTTGCTGGT GCA	153

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATTTTACCTG ATGACCCAGA TAAGAAACCA CAGGCAAAGC AGTTGCAGAC CAAGAAACCA	60
CAGGCAAAGC AGTTGCAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT	120
GCAAGAAAAG AAGTGCAAAG ACTTACTGGT GCA	153

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln

- 56 -

1 5 10 15
Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Ser Arg Asp Leu Ala Lys
 20 25 30
Arg Glu Ala Gln Arg Leu Cys Gly Ala
 35 40

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln
1 5 10 15
Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg
 20 25 30
Lys Glu Ala Gln Arg Leu Ala Gly Ala
 35 40

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ile	Leu	Pro	Asp	Asp	Pro	Asp	Lys	Lys	Pro	Gln	Ala	Lys	Gln	Leu	Gln
1				5					10					15	
Thr	Arg	Ala	Asp	Tyr	Leu	Ile	Lys	Leu	Leu	Asn	Lys	Asp	Leu	Ala	Arg
				20					25					30	
Lys	Glu	Ala	Gln	Arg	Leu	Ala	Gly	Ala							
				35					40						

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Ile	Leu	Pro	Asp	Asp	Pro	Asp	Lys	Lys	Pro	Gln	Ala	Lys	Gln	Leu	Gln
1					5					10				15	
Thr	Arg	Ala	Asp	Tyr	Leu	Ile	Lys	Leu	Leu	Asn	Lys	Asp	Leu	Ala	Arg
					20					25				30	
Lys	Glu	Val	Gln	Arg	Leu	Thr	Gly	Ala							
				35					40						

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6608 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CGGGCTGCGG CACGAAGCGC ACCGCCGGCG CACGCAGGCT CGGGCCGGGG AAGGCCTGGC	60
CCGCCGAGCC GGACGCACGC AGGTATTTGG GCAAAAATCT TGGCCATCTG TAGAGAATAG	120
CAAGTCAAAC GCATTACTTC GAAAACATAC GGAGTACCAG AAAGGGGATT CTTGACCTAC	180
ACCTTGTAAC CTGAGTGGAC TTTCTTTTTA ACTTCTTAAT ACTTACAATG AATGGGCACA	240
GTGATGAAGA AAGTGTAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG	300
GGTCAGCTTC AGGTTCTGGA TCTGGTTCAA GCTCTGGAAG CAGTAGCGAT GGAAGTAGCA	360
GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC AGGCAGTCAA TCCGAATCAG	420
AGTCTGACAC ATCTAGAGAG AAGAAACAAG TTCAAGCTAA ACCTCCGAAA GCTGACGGAT	480
CTGAGTTTTG GAAGTCCAGT CCAAGCATAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA	540
AGCAACAGCA ACAGCAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAGAG GACTCATCCA	600
GTAGTGAAGA TTCTGCCGAT GATTCGTCCA GTGAAACTAA GAAGAAAAAG CATAAAGATG	660
AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC TGGTTCTGAT TCTGAATCGG	720
CGGAAGATGG GGATAAAAGC AGTTGTGAAG AAAGTGAATC TGAATATGAG CCAAAAAACA	780
AAGTCAAAAG CCGTAAACCT CCAAGCAGAA TTAAGCCAAA AAGTGGGAAA AAGAGCACAG	840
GACAGAAGAA GAGGCAACTT GATTCATCAG AGGAGGAGGA GGACGATGAT GAAGATTATG	900
ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA GCTGAAGAAA	960
CCAAGACAGA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA GGATGTCCCA CAGACTGAAG	1020

AAGATGAATT	TGAAACTATA	GAGAAGTTTA	TGGACAGTCG	AATTGGCCGA	AAAGGAGCCA	1080
CTGGTGCCTC	AACCACCATC	TATGCCGTTG	AGGCAGATGG	TGACCCAAAT	GCTGGGTTTG	1140
AAAAGTCAAA	GGAGCTGGGA	GAAATACAGT	ATCTTATTAA	ATGGAAAGGC	TGGTCACACA	1200
TCCATAACAC	TTGGGAAACT	GAAGAAACGC	TGAAGCAACA	AAATGTTAAA	GGAATGAACA	1260
AACTGGACAA	CTACAAGAAA	AAGGATCAGG	AGACAAAACG	CTGGCTGAAA	AATGCTTCTC	1320
CAGAAGATGT	GGAATATTAT	AACTGCCAGC	AGGAGCTTAC	AGATGATCTG	CACAAACAAT	1380
ATCAAATAGT	GGAAAGAATA	ATTGCTCATT	CAAATCAAAA	GTCAGCAGCT	GGTTATCCGG	1440
ACTACTATTG	CAAATGGCAG	GGTCTGCCTT	ACTCAGAATG	TAGCTGGGAA	GATGGTGCTC	1500
TCATTGCCAA	AAAGTTTCAG	GCACGCATTG	ATGAGTATTT	TAGCAGAAAT	CAATCCAAGA	1560
CTACTCCCTT	TAAGGACTGC	AAGGTTCTAA	AACAGAGACC	AAGATTTGTT	GCACTGAAGA	1620
AGCAACCATC	TTACATTGGA	GGACATGAAA	GTCTGGAGTT	AAGAGATTAT	CAGTTAAATG	1680
GATTGAATTG	GCTCGCTCAT	TCATGGTGCA	AAGGAAATAG	TTGTATTCTT	GCAGATGAAA	1740
TGGGTCTGGG	TAAAACAATA	CAAACAATTT	CTTTTCTGAA	CTACCTGTTT	CATGAACATC	1800
AACTGTATGG	CCCTTTTCTT	CTGCGCGTGC	CACTTTCTAC	CTTGACATCT	TGGCAAAGAG	1860
AGATTCAAAC	TTGGGCTCCT	CAGATGAATG	CTGTAGTTTA	CTTAGGAGAT	ATAACTAGTA	1920
GAAATATGAT	AAGGACTCAT	GAATGGATGC	ATCCACAGAC	TAAACGATTA	AAGTTTAACA	1980
TACTTCTGAC	GACATATGAA	ATTTTACTGA	AGGATAAGTC	ATTCCTTGGT	GGTCTCAATT	2040
GGGCATT CAT	AGGAGTTGAT	GAAGCTCATC	GTTTAAAAAA	TGATGACTCT	CTTCTGTACA	2100
GGACTTTAAT	AGACTTTAAG	TCCAACCATC	GACTTCTGAT	TACTGGAACC	CCACTGCAAA	2160
ATTCCCTCAA	AGAGCTGTGG	TCTTTGTTGC	ATTTTCATCAT	GCCAGAAAAA	TTTTCCTCCT	2220
GGGAAGATTT	TGAAGAGGAG	CATGGCAAAG	GAAGAGAGTA	TGGTTATGCA	AGTCTTCACA	2280
AAGAGCTTGA	ACCATTTTTA	CTAAGAAGAG	TTAAAAAAGA	TGTAGAAAAG	TCTTTACCTG	2340
CTAAGGTTGA	ACAAATTCTG	AGGATGGAAA	TGAGTGCATT	GCAGAAGCAA	TATTACAAGT	2400
GGATTTTAAC	AAGGAATTAT	AAAGCCCTCA	GTAAAGGTTT	AAAAGGCAGT	ACCTCAGGCT	2460
TTCTGAACAT	TATGATGGAA	CTTAAGAAGT	GTTGTAACCA	TTGCTACCTC	ATTAAGCCAC	2520

CAGATGATAA TGAATTCTAT AATAAACAGG AGGCCTTACA GCATTTGATA CGTAGCAGCG	2580
GGAAACTAAT CCTTCTTGAC AAGCTACTGA TTCGTCTGCG AGAACGTGGC AACAGAGTTC	2640
TGATTTTCTC TCAGATGGTG AGGATGCTGG ACATCCTAGC AGAATATCTG AAGTATCGCC	2700
AGTTCCCTT CCAGAGACTT GATGGATCAA TAAAAGGGGA ATTGAGGAAG CAAGCACTGG	2760
ATCATTTCAA TGCAGAAGGA TCAGAGGATT TCTGTTTTTT ACTGTCTACA AGAGCTGGAG	2820
GATTAGGTAT TAACTTGGCA TCTGCTGACA CTGTAGTTAT TTTTGATTCT GACTGGAATC	2880
CACAGAATGA TCTGCAGGCA CAGGCGAGAG CTCATAGAAT TGGACAGAAG AAACAGGTTA	2940
ATATTTATCG GCTAGTCACA AAAGGATCAG TAGAAGAAGA TATTCTTGAA AGAGCCAAGA	3000
AGAAGATGGT GCTAGACCAT TTAGTAATTC AGAGAATGGA CACGACAGGA AAAACTGTTC	3060
TGCATACAGG TTCAACTCCA TCAAGCTCTA CACCTTTTAA TAAAGAAGAG TTATCAGCTA	3120
TTTTGAAGTT TGGTGCTGAG GAACTCTTTA AAGAACCTGA AGGAGAAGAA CAGGAGCCCC	3180
AGGAAATGGA TATAGATGAA ATCTTGAAGA GAGCTGAAAC TCGGGAAAAT GAGCCAGGTC	3240
CATTGACTGT AGGGGATGAG TTGCTTTCAC AGTTCAAGGT GGCGAACTTT TCCAATATGG	3300
ATGAAGATGA TATTGAGTTG GAACCAGAAA GAAATTCAAG AAATTGGGAA GAAATCATCC	3360
CAGAATCCCA ACGGAGAAGG ATAGAGGAGG AGGAAAGACA AAAAGAACTT GAAGAAATAT	3420
ACATGCTCCC GAGGATGAGA AACTGTGCAA AACAGATCAG CTTTAATGGG AGTGAAGGAA	3480
GACGCAGTAG GAGCAGAAGA TATTCTGGAT CTGATAGTGA CTCCATCACA GAAAGAAAAC	3540
GGCCAAAAAA GCGTGGAAGA CCTCGAACCA TTCCTCGAGA AAATATTAAA GGATTTAGTG	3600
ATGCAGAGAT CAGGCGGTTT ATCAAGAGTT ACAAGAAATT TGGTGGCCCT CTGGAAAGGT	3660
TAGATGCTGT AGCTAGAGAT GCTGAACTGG TTGATAAATC TGAGACAGAC CTTAGACGTT	3720
TGGGTGAACT TGTACATAAT GGATGCATTA AGGCTTTAAA GGACAATTCA TCTGGACAAG	3780
AAAGAGCAGG AGGTAGACTT GGGAAAGTTA AAGGCCCAAC GTTTCGAATC TCAGGAGTGC	3840
AGGTGAATGC AAAACTAGTC ATCTCTCAG AAGAAGAGCT GGCACCACTG CACAAATCCA	3900
TTCCTTCAGA TCCAGAAGAA AGGAAAAGAT ATGTCATCCC ATGCCACACC AAGGCTGCTC	3960
ACTTCGATAT AGATTGGGGT AAAGAAGATG ATTCCAATCT GTTAGTAGGC ATCTATGAAT	4020

ATGGCTATGG CAGCTGGGAA ATGATAAAAA TGGATCCAGA TCTCAGCTTA ACACAGAAGA	4080
TTTTACCTGA TGATCCAGAC AAGAAACCCC AGGCAAAGCA GCTACAGACC CGTGCAGACT	4140
ACCTCATTA ATTACTGAAT AAAGACCTTG CAAGAAAGGA AGCACAAAGG CTTGCTGGTG	4200
CAGGCAATTC CAAGAGAAGG AAGACAAGAA ATAAGAAGAA TAAGATGAAG GCTTCAAAAA	4260
TAAAAGAAGA AATAAAGAGT GATTCTTCAC CACAACCCTC AGAAAAATCT GATGAAGATG	4320
ATGAGGAGGA GGATAACAAG GTAAATGAAA TGAAATCTGA AAATAAAGAA AAATCTAAAA	4380
AAATTCCATT GCTGGATACT CCAGTTCATA TTACTGCAAC CAGTGAACCA GTTCCTATCT	4440
CAGAAGAATC TGAAGAACTC CATCAGAAGA CATTTAGTGT GTGCAAAGAA AGAATGAGGC	4500
CTGTCAAAGC AGCACTGAAA CAGCTGGATA GACCAGAGAA GGGCCTTTCT GAAAGGGAGC	4560
AGCTGGAACA TACTAGGCAG TGTCTAATCA AAATTGGGGA TCACATTACA GAATGCCTGA	4620
AGGAGTACAC AAATCCCGAG CAAATAAAAC AGTGGAGGAA AAATTTGTGG ATTTTGTGT	4680
CCAAGTTTAC AGAATTTGAT GCCAGAAAGC TGCACAACT CTACAAACAT GCAATCAAAA	4740
AGCGCCAAGA GTCTCAGCAA CACAATGACC AAAACATTAG CAGCAATGTG AATACACATG	4800
TAATCAGAAA TCCAGATGTG GAAAGACTGA AGGAGACTAC AAACCATGAT GATAGTAGCA	4860
GGGACAGTTA TTCTTCTGAT AGACATTTAT CACAATACCA TGATCATCAC AAAGACAGGC	4920
ATCAGGGAGA TGCTTACAAG AAAAGTGA CT CAGGAAAAAG GCCATATTCA GCCTTCAGTA	4980
ATGGAAAAGA TCACAGAGAC TGGGATCACT ACAAACAGGA CAGCAGATAC TACAGTGATA	5040
GTAAACATAG AAAGTTAGAT GACCACAGGA GCAGAGACCA CAGGTCAAAC CTGGAAGGAA	5100
ACTTAAAAGA CAGCCGGGGT CATTCAGATC ACCGCTCCCA TTCAGACCAC AGGATACACT	5160
CAGATCACCG TTCCACTTCA GAATACAGCC ATCATAAATC TTCGAGAGAT TATAGATACC	5220
ACTCAGACTG GCAAATGGAC CACAGAGCTT CTGGTAGTGG CCCGAGGTCA CCACTAGATC	5280
AGAGGTCTCC TTATGGTTCA AGATCTCCCC TAGGACACAG ATCTCCATTT GAACACTCAT	5340
CAGATCACA AAGTACACCT GAACATACAT GGAGTAGCCG GAAGACATAA CAAAGACTGA	5400
CATTTTCTGG ACCTTCTTTT TAGCCATATA CAGTAACTA ACACAGTAAT TGCCTTACAT	5460
GACTTGAAAG ATATGGACTG GATATTCTAT CAGTAGCAGT ATTGTTACTT CTTTCCAGGA	5520

TGCAAGGTCT ATTATCCCAA CAGAAGAAAA ATATTTTGT ATTTAAAGTT TATGCTGCAC	5580
TGTGCTGCAA ATGTTGTGGC ACTTTTTTTT TAAGAAATGG AAGATGTTTA CTTTTACAGG	5640
GACCTCAACA CTGCCCCTTT CAGACTGGAT CTTACTATAA AACTCTTCAT GTCAAAGTGG	5700
TTCTAGGCTG AACACAGATT AAATTATGTT TGTAATGAA CACTTAAACA CTGACCTGTG	5760
CTTATGTTTC AGGAAAGAAT GGGGGATTTA TTTTGTTTTA TTTCTTGGTA GAGAACTCTC	5820
AAGGACTTTG TTCACTTTCC AAAGCTACTT GTTTACATTG TACACTGCGA CCACCTTGCC	5880
GCTTTTCATC ACAAGCTTGA ATATTTAAAT TCTGTACCTA CAGTTGTAAA ATAGCCAGGA	5940
TTTCTCCTGT TTGTGATCAG TTATAATGCC TTTTATGAA ACAAACAAAC AAACAAAAAA	6000
CAATTAAAAA AAAAAACACA ACAAACCAA CAAATGGCTG TAAATTATTG TAAATTAATT	6060
AAATGAGCTT TTTTCCGTCA GGCTTTTTTT GGCTGTTTCT TCCCCAACA ACTCAGGCCT	6120
TCTTTTCACA AAGTCAGTAT ACTTACATGT TTTAATAAAA TATCTCGATG GAATCAGAAT	6180
GTAAAAATGG GGAAGGGAAT ATTTTATTCC ATTTAGTGCT CCTTTTTTAT TGGATACTTT	6240
TACATACCTG TTTTGGTTG TTTTATTTTA TTTTTTTTTT CTATTAAACT GTCAGTGTTG	6300
TGATTGTTGT AATGAACAGT GAGAATATCC CACTCTAAAC TGTGCCCTGG AAAGCTTTTC	6360
AGGTGCATTG GTTTAAAAGA AGGAAGTGTT CTATAGGTGA ACACTTCAAA ACCCAGATCA	6420
GCCAAGATTC ATTGTAAATC CATTTGTTTT CCCTCTTTAA CATGGGCAAT AATGTCAAAT	6480
GTGCTATGCA GCAGTTAATA TTTTAGAAGA TTTGAATGAC TTTATTAACA GAATTGTTAC	6540
AATGCACACT GATTGTACAT AGATAACTTC TATCTGACAA ATTAAATTAA CTAAAACCAA	6600
AAAAAACC	6608

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```
Asp Glu Ile Val Ser Val Lys His Leu His Lys Lys Ile Lys Thr Glu
1           5           10           15
Lys Glu Asn Glu Glu Lys Pro Glu Pro Asp Ile Gly Ile Lys Lys Glu
          20           25           30
Ala Glu Glu Lys Arg Glu Thr Lys Glu Lys Glu Asn Lys Arg Glu Leu
          35           40           45
Lys Arg Glu Lys Lys Glu Lys Glu Asp Lys Lys Glu Leu Lys Glu Lys
          50           55           60
Asp Asn Lys Glu Lys Arg Glu Asn Lys Val Lys Glu Ser Thr Gln Lys
65           70           75           80
Glu Lys Glu Val Lys Glu Glu Lys
          85
```

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GATGAGATTG TTTCAGTGAA ACATCTACAT AAAAAAATAA AAACAGAAAA AAGAAAATGA

AGAAAAGCCT GAGCCAGATA TTGGTATAAA GAAGGAAGCT GAAGAAAAAA GAGAGACAAA	120
AGAGAAGGAA AATAAAAGGG AATTGAAAAG GGAGAAAAAA GAAAAAGAGG ATAAGAAAGA	180
ATTAAAAGAA AAAGATAATA AAGAAAAGAG AGAAAACAAA GTAAAAGAAT CCACACAGAA	240
AGAAAAGAA GTGAAGGAAG AGAAG	265

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GATGGGATTG TTTCAGTGAA ACATCCACAT AAAAAAATAA AAGCAGAAAA AAGAAAATGA	60
AGAAAAAGAT GAGCCAGAGA TTGGTATAAA GAAGGAAGCT GGAGAAAAAA GAGAGACAAA	120
AGAAAAGGAA AATAAGA	137

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Asp Gly Ile Val Ser Val Lys His Pro His Lys Lys Ile Lys Ala Glu
 1 5 10 15
 Lys Glu Asn Glu Glu Lys Asp Glu Pro Glu Ile Gly Ile Lys Lys Glu
 20 25 30
 Ala Gly Glu Lys Arg Glu Thr Lys Glu Lys Glu Asn Lys
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATTTATCGGC TAGTCACAAA AGGATCAGTA GAAGAAGATA TTCTTGAAAG AGCCAAGAAA	60
AAGATGGTGT TAGATCATTT AGTGATTCAG AGAATGGACA CCACAGGGAA AACTGTACTA	120
CATACAGGCT CTACTCCTTC AAGCTCAACA CCTTTTAATA AGGAAGAGTT ATCAGCAATT	180
TTGAAGTTTG GTGCTGAGGA ACTTTTTTAAA GAACCTGAAN NNGAAGAAGA GGAGCCTCAG	240
GAGATGGATA TAGATGAAAT CCTGAAGAGG NCTGAAACTC GAGAAAATGA GTCAGGCCCA	300
TTAACTGTAG GAGATGAGTT ACTTTCACAG TTCAAGGTAG CTAACCTTTC CAATATGGAT	360
GAAGATGACA TTGAATTGGA ACCAGAACAA AATCTAAGAA ACTGGGAAGA AATCATTCCA	420
GAAGTTCAGT GGCGACGAAT AGAGGGGNGG GAAAGACAAA AAGAACTTGA AGAAATATAT	480
ATGCTTCCAA GAATGAGAAA CTGTGCAAAA CAGATCAGCT TTAATGGAAA TGAAGGGAGA	540

TGCAGTAGGA GCAGAAGATA TTCTGGATCT GATAGTGATT CCATCTCAGA AAGAAAACGA	600
CCAAAAAAAC GTGGACGACC ACGAACTATT CCCCCTGAAA ACATTAAAGG ATTTAGTGAT	660
GCAGAGATTA GACGATTTAT CAAGAGTTAC AAGAAATTTG GTGGCCCAGT TGAAAGGTTA	720
GATGCTATAG CTAGAGATGC TGAGCTAGTT GATAAATCTG AAACAGACCT TAGACGTCTG	780
GGAGAACTTG TACATAATGG ATGCATTAAG GCTTTAAATG ATAATGACTT TGGTCAAGGA	840
AGAACAGGTG GTAGATTTGG GAAAGTTAAA GGCCCAACAT TCCGAATAGC AGGAGTGCAG	900
GTGAATGCAA AGCTAGTCAT TTCTCACGAA GAAGAGTTGG CACCATTGCA TAAATCGATT	960
CCTTCAGATC CAGAAGAAAAG GAAAAGATAT GTCATCCCAT ACCACACCAA AGCAGCTCAT	1020
TTTGATATAG ATTGGGGTAA AGAAGATGAT TCCAATCTGT TAATAGGCAT CTATGAATAT	1080
GGTTATGGCA GTTGGGAAAT GATAAAAATG GATCCTGATC TCAGTTTGAC ACAGAAGATT	1140
TTACCTGATG ATCCAGATAA GAAACCCCAG GCTAAGCAGT TACAGACTCG TGCAGATTAC	1200
CTCATTAAT TACTGAATAA AGACCTTGCA AGAAAGGAAG CACAGAGACT TGCTGGTGCA	1260
GGCAATTCAA AGAGGAGAAA AACAAGAAGT AAGAAGAATA AAGCAACAAA GGCTGC	1316

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Asp Ala Arg Arg Tyr Leu Gly Lys Asn Leu Gly His Leu Arg Ile Ala

1

5

10

15

Ser Gln Thr His Tyr Phe Glu Asn Ile Arg Ser Thr Arg Lys Gly Ile

	20		25		30
Leu Asp	Leu His	Leu Val	Thr Val	Asp Phe	Leu Phe Asn Phe Leu Ile
35		40		45	
Leu Thr	Met Asn	Gly His	Ser Asp	Glu Glu	Ser Val Arg Asn Ser Ser
50		55		60	
Gly Glu	Ser Ser	Arg Ser	Asp Asp	Asp Ser	Ala Gly Ser Ala Ser Gly
65		70		75	80
Ser Gly	Ser Gly	Ser Ser	Ser Gly	Ser Ser	Ser Asp Gly Ser Ser Ser
	85		90		95
Gln Ser	Gly Ser	Ser Asp	Ser Glu	Ser Gly	Ser Glu Ser Gly Ser Gln
	100		105		110
Ser Glu	Ser Glu	Ser Asp	Thr Ser	Arg Glu	Lys Lys Gln Val Gln Ala
115		120		125	
Lys Pro	Pro Lys	Ala Asp	Gly Ser	Glu Phe	Trp Lys Ser Ser Pro Ser
130		135		140	
Ile Leu	Ala Val	Gln Arg	Ser Ala	Val Leu	Lys Lys Gln Gln Gln Gln
145		150		155	160
Gln Lys	Ala Ala	Ser Ser	Asp Ser	Gly Ser	Glu Glu Asp Ser Ser Ser
	165		170		175
Ser Glu	Asp Ser	Ala Asp	Asp Ser	Ser Ser	Ser Glu Thr Lys Lys Lys Lys
	180		185		190
His Lys	Asp Glu	Asp Trp	Gln Met	Ser Gly	Ser Gly Ser Val Ser Gly
	195		200		205
Thr Gly	Ser Asp	Ser Glu	Ser Ala	Glu Asp	Gly Asp Lys Ser Ser Cys
210		215		220	

Glu Glu Ser Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Lys Ser Arg
 225 230 235 240
 Lys Pro Pro Ser Arg Ile Lys Pro Lys Ser Gly Lys Lys Ser Thr Gly
 245 250 255
 Gln Lys Lys Arg Gln Leu Asp Ser Ser Glu Glu Glu Glu Asp Asp Asp
 260 265 270
 Glu Asp Tyr Asp Lys Arg Gly Ser Arg Arg Gln Ala Thr Val Asn Val
 275 280 285
 Ser Tyr Lys Glu Ala Glu Glu Thr Lys Thr Asp Ser Asp Asp Leu Leu
 290 295 300
 Glu Val Cys Gly Glu Asp Val Pro Gln Thr Glu Glu Asp Glu Phe Glu
 305 310 315 320
 Thr Ile Glu Lys Phe Met Asp Ser Arg Ile Gly Arg Lys Gly Ala Thr
 325 330 335
 Gly Ala Ser Thr Thr Ile Tyr Ala Val Glu Ala Asp Gly Asp Pro Asn
 340 345 350
 Ala Gly Phe Glu Lys Ser Lys Glu Leu Gly Glu Ile Gln Tyr Leu Ile
 355 360 365
 Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu
 370 375 380
 Thr Leu Lys Gln Gln Asn Val Lys Gly Met Asn Lys Leu Asp Asn Tyr
 385 390 395 400
 Lys Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro
 405 410 415
 Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu

420	425	430
His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser Asn Gln		
435	440	445
Lys Ser Ala Ala Gly Tyr Pro Asp Tyr Tyr Cys Lys Trp Gln Gly Leu		
450	455	460
Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ala Lys Lys		
465	470	475
Phe Gln Ala Arg Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser Lys Thr		480
485	490	495
Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg Phe Val		
500	505	510
Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Ser Leu Glu		
515	520	525
Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His Ser Trp		
530	535	540
Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu Gly Lys		
545	550	555
Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu His Gln		
565	570	575
Leu Tyr Gly Pro Phe Leu Leu Arg Val Pro Leu Ser Thr Leu Thr Ser		
580	585	590
Trp Gln Arg Glu Ile Gln Thr Trp Ala Pro Gln Met Asn Ala Val Val		
595	600	605
Tyr Leu Gly Asp Ile Thr Ser Arg Asn Met Ile Arg Thr His Glu Trp		
610	615	620

- 70 -

Met His Pro Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu Thr Thr
625 630 635 640
Tyr Glu Ile Leu Leu Lys Asp Lys Ser Phe Leu Gly Gly Leu Asn Trp
 645 650 655
Ala Phe Ile Gly Val Asp Glu Ala His Arg Leu Lys Asn Asp Asp Ser
 660 665 670
Leu Leu Tyr Arg Thr Leu Ile Asp Phe Lys Ser Asn His Arg Leu Leu
 675 680 685
Ile Thr Gly Thr Pro Leu Gln Asn Ser Leu Lys Glu Leu Trp Ser Leu
 690 695 700
Leu His Phe Ile Met Pro Glu Lys Phe Ser Ser Trp Glu Asp Phe Glu
705 710 715 720
Glu Glu His Gly Lys Gly Arg Glu Tyr Gly Tyr Ala Ser Leu His Lys
 725 730 735
Glu Leu Glu Pro Phe Leu Leu Arg Arg Val Lys Lys Asp Val Glu Lys
 740 745 750
Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met Ser Ala
 755 760 765
Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr Lys Ala
 770 775 780
Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn Ile Met
785 790 795 800
Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys Pro Pro
 805 810 815
Asp Asp Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His Leu Ile

820	825	830
Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile Arg Leu		
835	840	845
Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val Arg Met		
850	855	860
Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro Phe Gln		
865	870	875
Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala Leu Asp		
885	890	895
His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu Ser Thr		
900	905	910
Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr Val Val		
915	920	925
Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala Gln Ala		
930	935	940
Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr Arg Leu		
945	950	955
Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala Lys Lys		
965	970	975
Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr Thr Gly		
980	985	990
Lys Thr Val Leu His Thr Gly Ser Ala Pro Ser Ser Ser Thr Pro Phe		
995	1000	1005
Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu Glu Leu		
1010	1015	1020

Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met Asp Ile			
1025	1030	1035	1040
Asp Glu Ile Leu Lys Arg Ala Glu Thr His Glu Asn Glu Pro Gly Pro			
	1045	1050	1055
Leu Ser Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala Asn Phe			
	1060	1065	1070
Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg Asn Ser			
	1075	1080	1085
Lys Asn Trp Glu Glu Ile Ile Pro Glu Glu Gln Arg Arg Arg Leu Glu			
	1090	1095	1100
Glu Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr Met Leu Pro Arg			
1105	1110	1115	1120
Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly Ser Glu Gly Arg			
	1125	1130	1135
Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser Asp Ser Ile Ser			
	1140	1145	1150
Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile Pro Arg			
	1155	1160	1165
Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe Ile Lys			
	1170	1175	1180
Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala Ile Ala			
1185	1190	1195	1200
Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg Arg Leu			
	1205	1210	1215
Gly Glu Leu Val His Asn Gly Cys Val Lys Ala Leu Lys Asp Ser Ser			

1220	1225	1230	
Ser Gly Thr Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys Gly Pro			
1235	1240	1245	
Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val Ile Ala			
1250	1255	1260	
His Glu Asp Glu Leu Ile Pro Leu His Lys Ser Ile Pro Ser Asp Pro			
1265	1270	1275	1280
Glu Glu Arg Lys Gln Tyr Thr Ile Pro Cys His Thr Lys Ala Ala His			
1285	1290	1295	
Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu Ile Gly			
1300	1305	1310	
Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met Asp Pro			
1315	1320	1325	
Asp Leu Ser Leu Thr His Lys Ile Leu Pro Asp Asp Pro Asp Lys Lys			
1330	1335	1340	
Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile Lys Leu			
1345	1350	1355	1360
Leu Ser Arg Asp Leu Ala Lys Arg Glu Ala Gln Arg Leu Cys Gly Ala			
1365	1370	1375	
Gly Gly Ser Lys Arg Arg Lys Thr Arg Ala Lys Lys Ser Lys Ala Met			
1380	1385	1390	
Lys Ser Ile Lys Val Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro Leu			
1395	1400	1405	
Pro Ser Glu Lys Ser Asp Glu Asp Asp Asp Lys Leu Asn Asp Ser Lys			
1410	1415	1420	

Pro Glu Ser Lys Asp Arg Ser Lys Lys Ser Val Val Ser Asp Ala Pro
1425 1430 1435 1440
Val His Ile Thr Ala Ser Gly Glu Pro Val Pro Ile Ala Glu Glu Ser
 1445 1450 1455
Glu Glu Leu Asp Gln Lys Thr Phe Ser Ile Cys Lys Glu Arg Met Arg
 1460 1465 1470
Pro Val Lys Ala Ala Leu Lys Gln Leu Asp Arg Pro Glu Lys Gly Leu
 1475 1480 1485
Ser Glu Arg Glu Gln Leu Glu His Thr Arg Gln Cys Leu Ile Lys Ile
 1490 1495 1500
Gly Asp His Ile Thr Glu Cys Leu Lys Glu Tyr Ser Asn Pro Glu Gln
1505 1510 1515 1520
Ile Lys Gln Trp Arg Lys Asn Leu Trp Ile Phe Val Ser Lys Phe Thr
 1525 1530 1535
Glu Phe Asp Ala Arg Lys Leu His Lys Leu Tyr Lys His Ala Ile Lys
 1540 1545 1550
Lys Arg Gln Glu Ser Gln Gln Asn Ser Asp Gln Asn Ser Asn Val Ala
 1555 1560 1565
Thr Thr His Val Ile Arg Asn Pro Asp Met Glu Arg Leu Lys Glu Asn
 1570 1575 1580
Thr Asn His Asp Asp Ser Ser Arg Asp Ser Tyr Ser Ser Asp Arg His
1585 1590 1595 1600
Leu Ser Gln Tyr His Asp His His Lys Asp Arg His Gln Gly Asp Ser
 1605 1610 1615
Tyr Lys Lys Ser Asp Ser Arg Lys Arg Pro Tyr Ser Ser Phe Ser Asn

1620	1625	1630	
Gly Lys Asp His Arg Glu Trp Asp His Tyr Arg Gln Asp Ser Arg Tyr			
1635	1640	1645	
Tyr Ser Asp Arg Glu Lys His Arg Lys Leu Asp Asp His Arg Ser Arg			
1650	1655	1660	
Glu His Arg Pro Ser Leu Glu Gly Gly Leu Lys Asp Leu Asp Gln Arg			
1665	1670	1675	1680
Ser Pro Tyr Gly Ser Arg Ser Pro Phe Glu His Ser Ala Glu His Arg			
1685	1690	1695	
Ser Thr Pro Glu His Thr Trp Ser Ser Arg Lys Thr Xaa Gln Lys Leu			
1700	1705	1710	
Met Ser Leu Ser Ser Gly Thr Leu Phe Xaa Pro Leu Thr Xaa Leu Glu			
1715	1720	1725	
Arg Tyr Gly Leu Asp Ile Leu Ser Val Ala Val Leu Leu Leu Leu Ser			
1730	1735	1740	
Arg Met Gln Gly Leu Leu Ser Gln Gln Lys Lys Asn Ile Phe Val Phe			
1745	1750	1755	1760
Lys Val Tyr Ala Ala Leu Cys Cys Lys Cys Cys Gly Thr Phe Phe Leu			
1765	1770	1775	
Arg Asn Gly Arg Cys Leu Leu Leu Gln Gly Pro Gln His Cys Pro Phe			
1780	1785	1790	
Gln Thr Gly Ser Tyr Tyr Lys Thr Leu His Val Lys Val Val Leu Gly			
1795	1800	1805	
Xaa Thr Gln Ile Lys Leu Cys Leu Xaa Met Asn Thr Xaa Thr Leu Thr			
1810	1815	1820	

Cys Ala Tyr Val Ser Gly Lys Asn Gly Gly Phe Ile Leu Phe Tyr Phe			
1825	1830	1835	1840
Leu Val Glu Asn Ser Gln Gly Leu Cys Ser Leu Ser Lys Ala Thr Cys			
	1845	1850	1855
Leu His Cys Thr Leu Arg Pro Pro Cys Arg Phe Ser Ser Gln Ala Xaa			
	1860	1865	1870
Ile Phe Lys Phe Cys Thr Tyr Ser Cys Lys Ile Ala Arg Ile Ser Pro			
	1875	1880	1885
Val Cys Asp Gln Leu Xaa Cys Leu Phe Met Lys Gln Thr Asn Lys Gln			
	1890	1895	1900
Lys Thr Ile Lys Lys Lys Asn Thr Thr Lys Pro Thr Asn Gly Cys Lys			
1905	1910	1915	1920
Leu Leu Xaa Ile Asn Xaa Met Ser Phe Phe Pro Ser Gly Phe Phe Trp			
	1925	1930	1935
Leu Phe Leu Ser Pro Thr Thr Gln Ala Phe Phe Ser Gln Ser Gln Tyr			
	1940	1945	1950
Thr Tyr Met Phe Xaa Xaa Asn Ile Ser Met Glu Ser Glu Cys Lys Asn			
	1955	1960	1965
Gly Glu Gly Asn Ile Leu Phe His Leu Val Leu Leu Phe Tyr Trp Ile			
	1970	1975	1980
Leu Leu His Thr Cys Phe Trp Leu Phe Tyr Phe Ile Phe Phe Phe Tyr			
1985	1990	1995	2000
Xaa Thr Val Ser Val Val Ile Val Val Met Asn Ser Glu Asn Ile Pro			
	2005	2010	2015
Leu Xaa Thr Val Pro Trp Lys Ala Phe Gln Val His Trp Phe Lys Arg			

2020	2025	2030	
Arg Lys Cys Ser Ile Gly Glu His Phe Lys Thr Gln Ile Ser Gln Asp			
2035	2040	2045	
Ser Leu Xaa Ile His Leu Phe Ser Leu Phe Asn Met Gly Asn Asn Val			
2050	2055	2060	
Lys Cys Ala Met Gln Gln Leu Ile Phe Xaa Lys Ile Xaa Met Thr Leu			
2065	2070	2075	2080
Leu Thr Glu Leu Leu Gln Cys Thr Leu Ile Val His Arg Xaa Leu Leu			
2085	2090	2095	
Ser Asp Lys Leu Asn Xaa Leu Lys Pro Lys Lys Thr			
2100	2105		

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1795 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Phe	Ala	Leu	Cys	Pro	Pro	Val	Thr	Gln	Arg	Glu	Pro	Gln	Glu	Thr	Arg
1				5					10					15	
Glu Cys Arg Lys Phe Ile Phe Glu Ile Leu Ile Phe Glu Glu Ile Cys															
				20					25					30	
Ile His Thr His Leu Leu Leu Ile Gly Asp Phe Cys Phe Ile Asn Phe															

35	40	45
Leu Ile Phe Thr Met Asn Gly His Ser Asp Glu Glu Ser Val Arg Asn		
50	55	60
Gly Ser Gly Glu Ser Ser Gln Ser Gly Asp Asp Cys Gly Ser Ala Ser		
65	70	75
Gly Ser Gly Ser Gly Ser Ser Ser Gly Ser Ser Ser Asp Gly Ser Ser		
85	90	95
Ser Gln Ser Gly Ser Ser Asp Ser Asp Ser Gly Ser Asp Ser Gly Ser		
100	105	110
Gln Ser Glu Ser Glu Ser Asp Thr Ser Arg Glu Asn Lys Val Gln Ala		
115	120	125
Lys Pro Pro Lys Val Asp Gly Ala Glu Phe Trp Lys Ser Ser Pro Ser		
130	135	140
Ile Leu Ala Val Gln Arg Ser Ala Met Leu Arg Lys Gln Pro Gln Gln		
145	150	155
Ala Gln Gln Gln Arg Pro Ala Ser Ser Asn Ser Gly Ser Glu Glu Asp		
165	170	175
Ser Ser Ser Ser Glu Asp Ser Asp Asp Ser Ser Ser Gly Ala Lys Arg		
180	185	190
Lys Lys His Asn Asp Glu Asp Trp Gln Met Ser Gly Ser Gly Ser Pro		
195	200	205
Ser Gln Leu Gly Ser Asp Ser Glu Ser Glu Glu Glu Arg Asp Lys Ser		
210	215	220
Ser Cys Asp Gly Thr Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Arg		
225	230	235
		240

Ser Arg Lys Pro Gln Asn Arg Ser Lys Ser Lys Asn Gly Lys Lys Ile			
	245	250	255
Leu Gly Gln Lys Lys Arg Gln Ile Asp Ser Ser Glu Asp Glu Asp Asp			
	260	265	270
Glu Asp Tyr Asp Asn Asp Lys Arg Ser Ser Arg Arg Gln Ala Thr Val			
	275	280	285
Asn Val Ser Tyr Lys Glu Asp Glu Glu Met Lys Thr Asp Ser Asp Asp			
	290	295	300
Leu Leu Glu Val Cys Gly Glu Asp Val Pro Gln Pro Glu Asp Glu Glu			
	305	310	315
Phe Glu Thr Ile Glu Arg Val Met Asp Cys Arg Val Gly Arg Lys Gly			
	325	330	335
Ala Thr Gly Ala Thr Thr Thr Ile Tyr Ala Val Glu Ala Asp Gly Asp			
	340	345	350
Pro Asn Ala Gly Phe Glu Arg Asn Lys Glu Pro Gly Asp Ile Gln Tyr			
	355	360	365
Leu Ile Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr			
	370	375	380
Glu Glu Thr Leu Lys Gln Gln Asn Val Arg Gly Met Lys Lys Leu Asp			
	385	390	395
Asn Tyr Lys Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala			
	405	410	415
Ser Pro Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp			
	420	425	430
Asp Leu His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser			

435	440	445	
Asn Gln Lys Ser Ala Ala Gly Leu Pro Asp Tyr Tyr Cys Lys Trp Gln			
450	455	460	
Gly Leu Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ser			
465	470	475	480
Lys Lys Phe Gln Thr Cys Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser			
485	490	495	
Lys Thr Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg			
500	505	510	
Phe Val Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Gly			
515	520	525	
Leu Glu Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His			
530	535	540	
Ser Trp Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu			
545	550	555	560
Gly Lys Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu			
565	570	575	
His Gln Leu Tyr Gly Pro Phe Leu Leu Val Val Pro Leu Ser Thr Leu			
580	585	590	
Thr Ser Trp Gln Arg Glu Ile Gln Thr Trp Ala Ser Gln Met Asn Ala			
595	600	605	
Val Val Tyr Leu Gly Asp Ile Asn Ser Arg Asn Met Ile Arg Thr His			
610	615	620	
Glu Trp Met His Pro Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu			
625	630	635	640

Thr Thr Tyr Glu Ile Leu Leu Lys Asp Lys Ala Phe Leu Gly Gly Leu
645 650 655
Asn Trp Ala Phe Ile Gly Val Asp Glu Ala His Arg Leu Lys Asn Asp
660 665 670
Asp Ser Leu Leu Tyr Lys Thr Leu Ile Asp Phe Lys Ser Asn His Arg
675 680 685
Leu Leu Ile Thr Gly Thr Pro Leu Gln Asn Ser Leu Lys Glu Leu Trp
690 695 700
Ser Leu Leu His Phe Ile Met Pro Glu Lys Phe Ser Ser Trp Glu Asp
705 710 715 720
Phe Glu Glu Glu His Gly Lys Gly Arg Glu Tyr Gly Tyr Ala Ser Leu
725 730 735
His Lys Glu Leu Glu Pro Phe Leu Leu Arg Arg Val Lys Lys Asp Val
740 745 750
Glu Lys Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met
755 760 765
Ser Ala Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr
770 775 780
Lys Ala Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn
785 790 795 800
Ile Met Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys
805 810 815
Pro Pro Asp Asn Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His
820 825 830
Leu Ile Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile

835	840	845	
Arg Leu Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val			
850	855	860	
Arg Met Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro			
865	870	875	880
Phe Gln Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala			
885	890	895	
Leu Asp His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu			
900	905	910	
Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr			
915	920	925	
Val Val Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala			
930	935	940	
Gln Ala Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr			
945	950	955	960
Arg Leu Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala			
965	970	975	
Lys Lys Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr			
980	985	990	
Thr Gly Lys Thr Val Leu His Thr Gly Ser Thr Pro Ser Ser Ser Thr			
995	1000	1005	
Pro Phe Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu			
1010	1015	1020	
Glu Leu Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met			
1025	1030	1035	1040

Asp Ile Asp Glu Ile Leu Lys Arg Ala Glu Thr Arg Glu Asn Glu Pro
1045 1050 1055
Gly Pro Leu Thr Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala
1060 1065 1070
Asn Phe Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg
1075 1080 1085
Asn Ser Arg Asn Trp Glu Glu Ile Ile Pro Glu Ser Gln Arg Arg Arg
1090 1095 1100
Ile Glu Glu Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr Met Leu
1105 1110 1115 1120
Pro Arg Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly Ser Glu
1125 1130 1135
Gly Arg Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser Asp Ser
1140 1145 1150
Ile Thr Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile
1155 1160 1165
Pro Arg Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe
1170 1175 1180
Ile Lys Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala
1185 1190 1195 1200
Val Ala Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg
1205 1210 1215
Arg Leu Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu Lys Asp
1220 1225 1230
Asn Ser Ser Gly Gln Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys

1235	1240	1245	
Gly Pro Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val			
1250	1255	1260	
Ile Ser His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile Pro Ser			
1265	1270	1275	1280
Asp Pro Glu Glu Arg Lys Arg Tyr Val Ile Pro Cys His Thr Lys Ala			
1285	1290	1295	
Ala His Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu			
1300	1305	1310	
Val Gly Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met			
1315	1320	1325	
Asp Pro Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp Pro Asp			
1330	1335	1340	
Lys Lys Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile			
1345	1350	1355	1360
Lys Leu Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg Leu Ala			
1365	1370	1375	
Gly Ala Gly Asn Ser Lys Arg Arg Lys Thr Arg Asn Lys Lys Asn Lys			
1380	1385	1390	
Met Lys Ala Ser Lys Ile Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro			
1395	1400	1405	
Gln Pro Ser Glu Lys Ser Asp Glu Asp Asp Glu Glu Glu Asp Asn Lys			
1410	1415	1420	
Val Asn Glu Met Lys Ser Glu Asn Lys Glu Lys Ser Lys Lys Ile Pro			
1425	1430	1435	1440

Leu Leu Asp Thr Pro Val His Ile Thr Ala Thr Ser Glu Pro Val Pro
 1445 1450 1455
 Ile Ser Glu Glu Ser Glu Glu Leu His Gln Lys Thr Phe Ser Val Cys
 1460 1465 1470
 Lys Glu Arg Met Arg Pro Val Lys Ala Ala Leu Lys Gln Leu Asp Arg
 1475 1480 1485
 Pro Glu Lys Gly Leu Ser Glu Arg Glu Gln Leu Glu His Thr Arg Gln
 1490 1495 1500
 Cys Leu Ile Lys Ile Gly Asp His Ile Thr Glu Cys Leu Lys Glu Tyr
 1505 1510 1515 1520
 Thr Asn Pro Glu Gln Ile Lys Gln Trp Arg Lys Asn Leu Trp Ile Phe
 1525 1530 1535
 Val Ser Lys Phe Thr Glu Phe Asp Ala Arg Lys Leu His Lys Leu Tyr
 1540 1545 1550
 Lys His Ala Ile Lys Lys Arg Gln Glu Ser Gln Gln His Asn Asp Gln
 1555 1560 1565
 Asn Ile Ser Ser Asn Val Asn Thr His Val Ile Arg Asn Pro Asp Val
 1570 1575 1580
 Glu Arg Leu Lys Glu Thr Thr Asn His Asp Asp Ser Ser Arg Asp Ser
 1585 1590 1595 1600
 Tyr Ser Ser Asp Arg His Leu Ser Gln Tyr His Asp His His Lys Asp
 1605 1610 1615
 Arg His Gln Gly Asp Ala Tyr Lys Lys Ser Asp Ser Arg Lys Arg Pro
 1620 1625 1630
 Tyr Ser Ala Phe Ser Asn Gly Lys Asp His Arg Asp Trp Asp His Tyr

1635	1640	1645	
Lys Gln Asp Ser Arg Tyr Tyr Ser Asp Ser Lys His Arg Lys Leu Asp			
1650	1655	1660	
Asp His Arg Ser Arg Asp His Arg Ser Asn Leu Glu Gly Asn Leu Lys			
1665	1670	1675	1680
Asp Ser Arg Gly His Ser Asp His Arg Ser His Ser Asp His Arg Ile			
1685	1690	1695	
His Ser Asp His Arg Ser Thr Ser Glu Tyr Ser His His Lys Ser Ser			
1700	1705	1710	
Arg Asp Tyr Arg Tyr His Ser Asp Trp Gln Met Asp His Arg Ala Ser			
1715	1720	1725	
Gly Ser Gly Pro Arg Ser Pro Leu Asp Gln Arg Ser Pro Tyr Gly Ser			
1730	1735	1740	
Arg Ser Pro Leu Gly His Arg Ser Pro Phe Glu His Ser Ser Asp His			
1745	1750	1755	1760
Lys Ser Thr Pro Glu His Thr Trp Ser Ser Arg Lys Thr Xaa Gln Arg			
1765	1770	1775	
Leu Thr Phe Ser Gly Pro Ser Phe Xaa Pro Tyr Thr Val Asn Xaa His			
1780	1785	1790	
Ser Asn Cys			
1795			

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Lys	Thr	Xaa	Glu	Pro	Gly	Glu	Ile	Gln	Tyr	Leu	Ile	Lys	Trp	Lys	Gly
1				5					10					15	
Trp	Ser	His	Ile	His	Asn	Thr	Trp	Glu	Thr	Glu	Glu	Thr	Leu	Lys	Gln
			20					25					30		
Gln	Asn	Val	Arg	Gly	Met	Lys	Lys	Leu	Asp	Asn	Tyr	Lys	Lys	Lys	Asp
		35					40					45			
Gln	Glu	Thr	Lys	Arg	Trp	Leu	Lys	Asn	Ala	Ser	Pro	Glu	Asp	Val	Glu
		50					55					60			
Tyr	Tyr	Asn	Cys	Gln	Gln	Glu	Leu	Thr	Asp	Asp	Leu	His	Lys	Gln	Tyr
65					70					75				80	
Gln	Ile	Val	Glu	Arg	Thr	Asn	Xaa	Ser	Phe	Gln	Ser	Lys	Ser	Ala	Ala
					85					90				95	
Gly	Tyr	Pro													

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 439 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Ile Tyr Arg Leu Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu
1 5 10 15
Arg Ala Lys Lys Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met
 20 25 30
Asp Thr Thr Gly Lys Thr Val Leu His Thr Gly Ser Thr Pro Ser Ser
 35 40 45
Ser Thr Pro Phe Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly
 50 55 60
Ala Glu Glu Leu Phe Lys Glu Pro Glu Xaa Glu Glu Glu Glu Pro Gln
65 70 75 80
Glu Met Asp Ile Asp Glu Ile Leu Lys Arg Xaa Glu Thr Arg Glu Asn
 85 90 95
Glu Ser Gly Pro Leu Thr Val Gly Asp Glu Leu Leu Ser Gln Phe Lys
 100 105 110
Val Ala Asn Phe Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro
 115 120 125
Glu Gln Asn Leu Arg Asn Trp Glu Glu Ile Ile Pro Glu Val Gln Trp
 130 135 140
Arg Arg Ile Glu Gly Xaa Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr
145 150 155 160
Met Leu Pro Arg Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly
 165 170 175
Asn Glu Gly Arg Cys Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser

180	185	190
Asp Ser Ile Ser Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg		
195	200	205
Thr Ile Pro Arg Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg		
210	215	220
Arg Phe Ile Lys Ser Tyr Lys Lys Phe Gly Gly Pro Val Glu Arg Leu		
225	230	235
240		
Asp Ala Ile Ala Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp		
245	250	255
Leu Arg Arg Leu Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu		
260	265	270
Asn Asp Asn Asp Phe Gly Gln Gly Arg Thr Gly Gly Arg Phe Gly Lys		
275	280	285
Val Lys Gly Pro Thr Phe Arg Ile Ala Gly Val Gln Val Asn Ala Lys		
290	295	300
Leu Val Ile Ser His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile		
305	310	315
320		
Pro Ser Asp Pro Glu Glu Arg Lys Arg Tyr Val Ile Pro Tyr His Thr		
325	330	335
Lys Ala Ala His Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn		
340	345	350
Leu Leu Ile Gly Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile		
355	360	365
Lys Met Asp Pro Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp		
370	375	380

Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr
385 390 395 400
Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg
 405 410 415
Leu Ala Gly Ala Gly Asn Ser Lys Arg Arg Lys Thr Arg Ser Lys Lys
 420 425 430
Asn Lys Ala Thr Lys Ala Ala
 435

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1434 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..1434
- (D) OTHER INFORMATION: /note= "The sequence beginning at 1
corresponds to 55 and that ending at 1434 corresponds to

1488"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Lys Pro Pro Lys Ala Asp Gly Ser Glu Phe Trp Lys Ser Ser Pro Ser

1

5

10

15

Ile	Leu	Ala	Val	Gln	Arg	Ser	Ala	Val	Leu	Lys	Lys	Gln	Gln	Gln	Gln
			20					25					30		
Gln	Lys	Ala	Ala	Ser	Ser	Asp	Ser	Gly	Ser	Glu	Glu	Asp	Ser	Ser	Ser
		35					40					45			
Ser	Glu	Asp	Ser	Ala	Asp	Asp	Ser	Ser	Ser	Glu	Thr	Lys	Lys	Lys	Lys
	50					55						60			
His	Lys	Asp	Glu	Asp	Trp	Gln	Met	Ser	Gly	Ser	Gly	Ser	Val	Ser	Gly
65					70					75				80	
Thr	Gly	Ser	Asp	Ser	Glu	Ser	Ala	Glu	Asp	Gly	Asp	Lys	Ser	Ser	Cys
			85						90				95		
Glu	Glu	Ser	Glu	Ser	Asp	Tyr	Glu	Pro	Lys	Asn	Lys	Val	Lys	Ser	Arg
			100						105				110		
Lys	Pro	Pro	Ser	Arg	Ile	Lys	Pro	Lys	Ser	Gly	Lys	Lys	Ser	Thr	Gly
			115						120				125		
Gln	Lys	Lys	Arg	Gln	Leu	Asp	Ser	Ser	Glu	Glu	Glu	Glu	Asp	Asp	Asp
		130					135					140			
Glu	Asp	Tyr	Asp	Lys	Arg	Gly	Ser	Arg	Arg	Gln	Ala	Thr	Val	Asn	Val
145					150					155				160	
Ser	Tyr	Lys	Glu	Ala	Glu	Glu	Thr	Lys	Thr	Asp	Ser	Asp	Asp	Leu	Leu
				165						170				175	
Glu	Val	Cys	Gly	Glu	Asp	Val	Pro	Gln	Thr	Glu	Glu	Asp	Glu	Phe	Glu
			180						185				190		
Thr	Ile	Glu	Lys	Phe	Met	Asp	Ser	Arg	Ile	Gly	Arg	Lys	Gly	Ala	Thr
		195							200				205		
Gly	Ala	Ser	Thr	Thr	Ile	Tyr	Ala	Val	Glu	Ala	Asp	Gly	Asp	Pro	Asn

210 215 220
Ala Gly Phe Glu Lys Ser Lys Glu Leu Gly Glu Ile Gln Tyr Leu Ile
225 230 235 240
Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu
245 250 255
Thr Leu Lys Gln Gln Asn Val Lys Gly Met Asn Lys Leu Asp Asn Tyr
260 265 270
Lys Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro
275 280 285
Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu
290 295 300
His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser Asn Gln
305 310 315 320
Lys Ser Ala Ala Gly Tyr Pro Asp Tyr Tyr Cys Lys Trp Gln Gly Leu
325 330 335
Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ala Lys Lys
340 345 350
Phe Gln Ala Arg Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser Lys Thr
355 360 365
Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg Phe Val
370 375 380
Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Ser Leu Glu
385 390 395 400
Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His Ser Trp
405 410 415

Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu Gly Lys

420

425

430

Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu His Gln

435

440

445

Leu Tyr Gly Pro Phe Leu Leu Arg Val Pro Leu Ser Thr Leu Thr Ser

450

455

460

Trp Gln Arg Glu Ile Gln Thr Trp Ala Pro Gln Met Asn Ala Val Val

465

470

475

480

Tyr Leu Gly Asp Ile Thr Ser Arg Asn Met Ile Arg Thr His Glu Trp

485

490

495

Met His Pro Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu Thr Thr

500

505

510

Tyr Glu Ile Leu Leu Lys Asp Lys Ser Phe Leu Gly Gly Leu Asn Trp

515

520

525

Ala Phe Ile Gly Val Asp Glu Ala His Arg Leu Lys Asn Asp Asp Ser

530

535

540

Leu Leu Tyr Arg Thr Leu Ile Asp Phe Lys Ser Asn His Arg Leu Leu

545

550

555

560

Ile Thr Gly Thr Pro Leu Gln Asn Ser Leu Lys Glu Leu Trp Ser Leu

565

570

575

Leu His Phe Ile Met Pro Glu Lys Phe Ser Ser Trp Glu Asp Phe Glu

580

585

590

Glu Glu His Gly Lys Gly Arg Glu Tyr Gly Tyr Ala Ser Leu His Lys

595

600

605

Glu Leu Glu Pro Phe Leu Leu Arg Arg Val Lys Lys Asp Val Glu Lys

610	615	620	
Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met Ser Ala			
625	630	635	640
Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr Lys Ala			
	645	650	655
Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn Ile Met			
	660	665	670
Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys Pro Pro			
	675	680	685
Asp Asp Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His Leu Ile			
	690	695	700
Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile Arg Leu			
705	710	715	720
Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val Arg Met			
	725	730	735
Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro Phe Gln			
	740	745	750
Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala Leu Asp			
	755	760	765
His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu Ser Thr			
	770	775	780
Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr Val Val			
785	790	795	800
Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala Gln Ala			
	805	810	815

Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr Arg Leu
820 825 830
Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala Lys Lys
835 840 845
Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr Thr Gly
850 855 860
Lys Thr Val Leu His Thr Gly Ser Thr Pro Ser Ser Ser Thr Pro Phe
865 870 875 880
Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu Glu Leu
885 890 895
Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met Asp Ile
900 905 910
Asp Glu Ile Leu Lys Arg Ala Glu Thr Arg Glu Asn Glu Pro Gly Pro
915 920 925
Leu Thr Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala Asn Phe
930 935 940
Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg Asn Ser
945 950 955 960
Arg Asn Trp Glu Glu Ile Ile Pro Glu Ser Gln Arg Arg Arg Ile Glu
965 970 975
Glu Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr Met Leu Pro Arg
980 985 990
Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly Ser Glu Gly Arg
995 1000 1005
Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser Asp Ser Ile Thr

1010	1015	1020	
Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile Pro Arg			
1025	1030	1035	1040
Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe Ile Lys			
1045	1050	1055	
Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala Val Ala			
1060	1065	1070	
Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg Arg Leu			
1075	1080	1085	
Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu Lys Asp Asn Ser			
1090	1095	1100	
Ser Gly Gln Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys Gly Pro			
1105	1110	1115	1120
Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val Ile Ser			
1125	1130	1135	
His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile Pro Ser Asp Pro			
1140	1145	1150	
Glu Glu Arg Lys Arg Tyr Val Ile Pro Cys His Thr Lys Ala Ala His			
1155	1160	1165	
Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu Val Gly			
1170	1175	1180	
Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met Asp Pro			
1185	1190	1195	1200
Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp Pro Asp Lys Lys			
1205	1210	1215	

Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile Lys Leu

1220

1225

1230

Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg Leu Ala Gly Ala

1235

1240

1245

Gly Asn Ser Lys Arg Arg Lys Thr Arg Asn Lys Lys Asn Lys Met Lys

1250

1255

1260

Ala Ser Lys Ile Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro Gln Pro

1265

1270

1275

1280

Ser Glu Lys Ser Asp Glu Asp Asp Glu Glu Glu Asp Asn Lys Val Asn

1285

1290

1295

Glu Met Lys Ser Glu Asn Lys Glu Lys Ser Lys Lys Ile Pro Leu Leu

1300

1305

1310

Asp Thr Pro Val His Ile Thr Ala Thr Ser Glu Pro Val Pro Ile Ser

1315

1320

1325

Glu Glu Ser Glu Glu Leu His Gln Lys Thr Phe Ser Val Cys Lys Glu

1330

1335

1340

Arg Met Arg Pro Val Lys Ala Ala Leu Lys Gln Leu Asp Arg Pro Glu

1345

1350

1355

1360

Lys Gly Leu Ser Glu Arg Glu Gln Leu Glu His Thr Arg Gln Cys Leu

1365

1370

1375

Ile Lys Ile Gly Asp His Ile Thr Glu Cys Leu Lys Glu Tyr Thr Asn

1380

1385

1390

Pro Glu Gln Ile Lys Gln Trp Arg Lys Asn Leu Trp Ile Phe Val Ser

1395

1400

1405

Lys Phe Thr Glu Phe Asp Ala Arg Lys Leu His Lys Leu Tyr Lys His

1410	1415	1420
Ala Ile Lys Lys Arg Gln Glu Ser Gln Gln		
1425	1430	

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1467 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:1..1467

(D) OTHER INFORMATION:/note= "The sequence beginning at 1

corresponds to 2654 and that ending at 1467 corresponds to

4120"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met Ala Ala Lys Asp Ile Ser Thr Glu Val Leu Gln Asn Pro Glu Leu

1	5	10	15
---	---	----	----

Tyr Gly Leu Arg Arg Ser His Arg Ala Ala Ala His Gln Gln Asn Tyr

20	25	30
----	----	----

Phe Asn Asp Ser Asp Asp Glu Asp Asp Glu Asp Asn Ile Lys Gln Ser

35	40	45
----	----	----

Arg Arg Lys Arg Met Thr Thr Ile Glu Asp Asp Glu Asp Glu Phe Glu

50	55	60	
Asp Glu Glu Gly Glu Glu Asp Ser Gly Glu Asp Glu Asp Glu Glu Asp			
65	70	75	80
Phe Glu Glu Asp Asp Asp Tyr Tyr Gly Ser Pro Ile Lys Gln Asn Arg			
85	90	95	
Ser Lys Pro Lys Ser Arg Thr Lys Ser Lys Ser Lys Ser Lys Pro Lys			
100	105	110	
Ser Gln Ser Glu Lys Gln Ser Thr Val Lys Ile Pro Thr Arg Phe Ser			
115	120	125	
Asn Arg Gln Asn Lys Thr Val Asn Tyr Asn Ile Asp Tyr Ser Asp Asp			
130	135	140	
Asp Leu Leu Glu Ser Glu Asp Asp Tyr Gly Ser Glu Glu Ala Leu Ser			
145	150	155	160
Glu Glu Asn Val His Glu Ala Ser Ala Asn Pro Gln Pro Glu Asp Phe			
165	170	175	
His Gly Ile Asp Ile Val Ile Asn His Arg Leu Lys Thr Ser Leu Glu			
180	185	190	
Glu Gly Lys Val Leu Glu Lys Thr Val Pro Asp Leu Asn Asn Cys Lys			
195	200	205	
Glu Asn Tyr Glu Phe Leu Ile Lys Trp Thr Asp Glu Ser His Leu His			
210	215	220	
Asn Thr Trp Glu Thr Tyr Glu Ser Ile Gly Gln Val Arg Gly Leu Lys			
225	230	235	240
Arg Leu Asp Asn Tyr Cys Lys Gln Phe Ile Ile Glu Asp Gln Gln Val			
245	250	255	

Arg Leu Asp Pro Tyr Val Thr Ala Glu Asp Ile Glu Ile Met Asp Met

260

265

270

Glu Arg Glu Arg Arg Leu Asp Glu Phe Glu Glu Phe His Val Pro Glu

275

280

285

Arg Ile Ile Asp Ser Gln Arg Ala Ser Leu Glu Asp Gly Thr Ser Gln

290

295

300

Leu Gln Tyr Leu Val Lys Trp Arg Arg Leu Asn Tyr Asp Glu Ala Thr

305

310

315

320

Trp Glu Asn Ala Thr Asp Ile Val Lys Leu Ala Pro Glu Gln Val Lys

325

330

335

His Phe Gln Asn Arg Glu Asn Ser Lys Ile Leu Pro Gln Tyr Ser Ser

340

345

350

Asn Tyr Thr Ser Gln Arg Pro Arg Phe Glu Lys Leu Ser Val Gln Pro

355

360

365

Pro Phe Ile Lys Gly Gly Glu Leu Arg Asp Phe Gln Leu Thr Gly Ile

370

375

380

Asn Trp Met Ala Phe Leu Trp Ser Lys Gly Asp Asn Gly Ile Leu Ala

385

390

395

400

Asp Glu Met Gly Leu Gly Lys Thr Val Gln Thr Val Ala Phe Ile Ser

405

410

415

Trp Leu Ile Phe Ala Arg Arg Gln Asn Gly Pro His Ile Ile Val Val

420

425

430

Pro Leu Ser Thr Met Pro Ala Trp Leu Asp Thr Phe Glu Lys Trp Ala

435

440

445

Pro Asp Leu Asn Cys Ile Cys Tyr Met Gly Asn Gln Lys Ser Arg Asp

450	455	460
Thr Ile Arg Glu Tyr Glu Phe Tyr Thr Asn Pro Arg Ala Lys Gly Lys		
465	470	475
Lys Thr Met Lys Phe Asn Val Leu Leu Thr Thr Tyr Glu Tyr Ile Leu		480
485	490	495
Lys Asp Arg Ala Glu Leu Gly Ser Ile Lys Trp Gln Phe Met Ala Val		
500	505	510
Asp Glu Ala His Arg Leu Lys Asn Ala Glu Ser Ser Leu Tyr Glu Ser		
515	520	525
Leu Asn Ser Phe Lys Val Ala Asn Arg Met Leu Ile Thr Gly Thr Pro		
530	535	540
Leu Gln Asn Asn Ile Lys Glu Leu Ala Ala Leu Val Asn Phe Leu Met		
545	550	555
Pro Gly Arg Phe Thr Ile Asp Gln Glu Ile Asp Phe Glu Asn Gln Asp		560
565	570	575
Glu Glu Gln Glu Glu Tyr Ile His Asp Leu His Arg Arg Ile Gln Pro		
580	585	590
Phe Ile Leu Arg Arg Leu Lys Lys Asp Val Glu Lys Ser Leu Pro Ser		
595	600	605
Lys Thr Glu Arg Ile Leu Arg Val Glu Leu Ser Asp Val Gln Thr Glu		
610	615	620
Tyr Tyr Lys Asn Ile Leu Thr Lys Asn Tyr Ser Ala Leu Thr Ala Gly		
625	630	635
Ala Lys Gly Gly His Phe Ser Leu Leu Asn Ile Met Asn Glu Leu Lys		640
645	650	655

Lys Ala Ser Asn His Pro Tyr Leu Phe Asp Asn Ala Glu Glu Arg Val
660 665 670

Leu Gln Lys Phe Gly Asp Gly Lys Met Thr Arg Glu Asn Val Leu Arg
675 680 685

Gly Leu Ile Met Ser Ser Gly Lys Met Val Leu Leu Asp Gln Leu Leu
690 695 700

Thr Arg Leu Lys Lys Asp Gly His Arg Val Leu Ile Phe Ser Gln Met
705 710 715 720

Val Arg Met Leu Asp Ile Leu Gly Asp Tyr Leu Ser Ile Lys Gly Ile
725 730 735

Asn Phe Gln Arg Leu Asp Gly Thr Val Pro Ser Ala Gln Arg Arg Ile
740 745 750

Ser Ile Asp His Phe Asn Ser Pro Asp Ser Asn Asp Phe Val Phe Leu
755 760 765

Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Met Thr Ala Asp
770 775 780

Thr Val Val Ile Phe Asp Ser Asp Trp Asn Pro Gln Ala Asp Leu Gln
785 790 795 800

Ala Met Ala Arg Ala His Arg Ile Gly Gln Lys Asn His Val Met Val
805 810 815

Tyr Arg Leu Val Ser Lys Asp Thr Val Glu Glu Glu Val Leu Glu Arg
820 825 830

Ala Arg Lys Lys Met Ile Leu Glu Tyr Ala Ile Ile Ser Leu Gly Val
835 840 845

Thr Asp Gly Asn Lys Tyr Thr Lys Lys Asn Glu Pro Asn Ala Gly Glu

850	855	860	
Leu Ser Ala Ile Leu Lys Phe Gly Ala Gly Asn Met Phe Thr Ala Thr			
865	870	875	880
Asp Asn Gln Lys Lys Leu Glu Asp Leu Asn Leu Asp Asp Val Leu Asn			
	885	890	895
His Ala Glu Asp His Val Thr Thr Pro Asp Leu Gly Glu Ser His Leu			
	900	905	910
Gly Gly Glu Glu Phe Leu Lys Gln Phe Glu Val Thr Asp Tyr Lys Ala			
	915	920	925
Asp Ile Asp Trp Asp Asp Ile Ile Pro Glu Glu Glu Leu Lys Lys Leu			
	930	935	940
Gln Asp Glu Glu Gln Lys Arg Lys Asp Glu Glu Tyr Val Lys Glu Gln			
945	950	955	960
Leu Glu Met Met Asn Arg Arg Asp Asn Ala Leu Lys Lys Ile Lys Asn			
	965	970	975
Ser Val Asn Gly Asp Gly Thr Ala Ala Asn Ser Asp Ser Asp Asp Asp			
	980	985	990
Ser Thr Ser Arg Ser Ser Arg Arg Arg Ala Arg Ala Asn Asp Met Asp			
	995	1000	1005
Ser Ile Gly Glu Ser Glu Val Arg Ala Leu Tyr Lys Ala Ile Leu Lys			
	1010	1015	1020
Phe Gly Asn Leu Lys Glu Ile Leu Asp Glu Leu Ile Ala Asp Gly Thr			
1025	1030	1035	1040
Leu Pro Val Lys Ser Phe Glu Lys Tyr Gly Glu Thr Tyr Asp Glu Met			
	1045	1050	1055

- 104 -

Met Glu Ala Ala Lys Asp Cys Val His Glu Glu Glu Lys Asn Arg Lys			
1060	1065	1070	
Glu Ile Leu Glu Lys Leu Glu Lys His Ala Thr Ala Tyr Arg Ala Lys			
1075	1080	1085	
Leu Lys Ser Gly Glu Ile Lys Ala Glu Asn Gln Pro Lys Asp Asn Pro			
1090	1095	1100	
Leu Thr Arg Leu Ser Leu Lys Lys Arg Glu Lys Lys Ala Val Leu Phe			
1105	1110	1115	1120
Asn Phe Lys Gly Val Lys Ser Leu Asn Ala Glu Ser Leu Leu Ser Arg			
1125	1130	1135	
Val Glu Asp Leu Lys Tyr Leu Lys Asn Leu Ile Asn Ser Asn Tyr Lys			
1140	1145	1150	
Asp Asp Pro Leu Lys Phe Ser Leu Gly Asn Asn Thr Pro Lys Pro Val			
1155	1160	1165	
Gln Asn Trp Ser Ser Asn Trp Thr Lys Glu Glu Asp Glu Lys Leu Leu			
1170	1175	1180	
Ile Gly Val Phe Lys Tyr Gly Tyr Gly Ser Trp Thr Gln Ile Arg Asp			
1185	1190	1195	1200
Asp Pro Phe Leu Gly Ile Thr Asp Lys Ile Phe Leu Asn Glu Val His			
1205	1210	1215	
Asn Pro Val Ala Lys Lys Ser Ala Ser Ser Ser Asp Thr Thr Pro Thr			
1220	1225	1230	
Pro Ser Lys Lys Gly Lys Gly Ile Thr Gly Ser Ser Lys Lys Val Pro			
1235	1240	1245	
Gly Ala Ile His Leu Gly Arg Arg Val Asp Tyr Leu Leu Ser Phe Leu			

1250	1255	1260	
Arg Gly Gly Leu Asn Thr Lys Ser Pro Ser Ala Asp Ile Gly Ser Lys			
1265	1270	1275	1280
Lys Leu Pro Thr Gly Pro Ser Lys Lys Arg Gln Arg Lys Pro Ala Asn			
	1285	1290	1295
His Ser Lys Ser Met Thr Pro Glu Ile Thr Ser Ser Glu Pro Ala Asn			
	1300	1305	1310
Gly Pro Pro Ser Lys Arg Met Lys Ala Leu Pro Lys Gly Pro Ala Ala			
	1315	1320	1325
Leu Ile Asn Asn Thr Arg Leu Ser Pro Asn Ser Pro Thr Pro Pro Leu			
	1330	1335	1340
Lys Ser Lys Val Ser Arg Asp Asn Gly Thr Arg Gln Ser Ser Asn Pro			
1345	1350	1355	1360
Ser Ser Gly Ser Ala His Glu Lys Glu Tyr Asp Ser Met Asp Glu Glu			
	1365	1370	1375
Asp Cys Arg His Thr Met Ser Ala Ile Arg Thr Ser Leu Lys Arg Leu			
	1380	1385	1390
Arg Arg Gly Gly Lys Ser Leu Asp Arg Lys Glu Trp Ala Lys Ile Leu			
	1395	1400	1405
Lys Thr Glu Leu Thr Thr Ile Gly Asn His Ile Glu Ser Gln Lys Gly			
	1410	1415	1420
Ser Ser Arg Lys Ala Ser Pro Glu Lys Tyr Arg Lys His Leu Trp Ser			
1425	1430	1435	1440
Tyr Ser Ala Asn Phe Trp Pro Ala Asp Val Lys Ser Thr Lys Leu Met			
	1445	1450	1455

Ala Met Tyr Asp Lys Ile Thr Glu Ser Gln Lys

1460

1465

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Val Glu Ala Asp Gly Asp Pro Asn Ala Gly Phe Glu Lys Ser Lys

1 5 10 15

Glu Leu Gly Glu Ile Gln Tyr Leu Ile Lys Trp Lys Gly Trp Ser His

20 25 30

Ile His Asn Thr Trp Glu Thr Glu Glu Thr Leu Lys Gln Gln Asn Val

35 40 45

Lys Gly Met Asn Lys Leu Asp Asn Tyr Lys Lys

50

55

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Ala	Val	Glu	Ala	Asp	Gly	Asp	Pro	Asn	Ala	Gly	Phe	Glu	Arg	Asn	Lys
1				5					10					15	
Glu	Pro	Gly	Asp	Ile	Gln	Tyr	Leu	Ile	Lys	Trp	Lys	Gly	Trp	Ser	His
			20					25					30		
Ile	His	Asn	Thr	Trp	Glu	Thr	Glu	Glu	Thr	Leu	Lys	Gln	Gln	Asn	Val
		35					40						45		
Arg	Gly	Asn	Lys	Lys	Leu	Asp	Asn	Tyr	Lys	Lys					
		50					55								

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Glu	Gly	Lys	Val	Leu	Glu	Lys	Thr	Val	Pro	Asp	Leu	Asn	Asn	Cys	Lys
1				5					10					15	
Glu	Asn	Tyr	Glu	Phe	Leu	Ile	Lys	Trp	Thr	Asp	Glu	Ser	His	Leu	His
			20					25					30		
Asn	Thr	Trp	Glu	Thr	Tyr	Glu	Ser	Ile	Gly	Gln	Val	Arg	Gly	Leu	Lys

35 40 45
Arg Leu Asp Asn Tyr Cys Lys
50 55

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Glu Glu Glu Glu Glu Tyr Ala Val Glu Lys Ile Ile Asp Arg Arg Val
1 5 10 15
Arg Lys Gly Lys Val Glu Tyr Tyr Leu Lys Trp Lys Gly Tyr Pro Glu
20 25 30
Thr Glu Asn Thr Trp Glu Pro Glu Asn Asn Leu Asp Cys Gln Asp Leu
35 40 45
Ile Gln Gln Tyr
50

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Asp Glu Glu Glu Tyr Val Val Glu Lys Val Leu Asp Arg Arg Val

1 5 10 15

Val Lys Gly Lys Gln Val Glu Tyr Leu Leu Lys Trp Lys Gly Phe Ser

20 25 30

Glu Glu His Asn Thr Trp Glu Pro Glu Lys Asn Leu Asp Cys Pro Glu

35 40 45

Leu Ile Ser Glu Phe

50

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Glu Glu Glu Glu Glu Tyr Val Val Glu Lys Val Leu Asp Arg Arg Val

1 5 10 15

Val Lys Gly Lys Val Glu Tyr Leu Leu Lys Trp Lys Gly Phe Ser Asp

20

25

30

Glu Asp Asn Thr Trp Glu Pro Glu Glu Asn Leu Asp Cys Pro Asp Leu

35

40

45

Ile Ala Glu Phe

50

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Ala Glu Pro Glu Glu Phe Val Val Glu Lys Val Leu Asp Arg Arg Val

1

5

10

15

Val Asn Gly Lys Val Glu Tyr Phe Leu Lys Trp Lys Gly Phe Thr Asp

20

25

30

Ala Asp Asn Thr Trp Glu Pro Glu Glu Asn Leu Asp Cys Pro Glu Leu

35

40

45

Ile Glu Asp Phe

50

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Pro Val Asp Leu Val Tyr Ala Ala Glu Lys Ile Ile Gln Lys Arg Val
1 5 10 15
Lys Lys Gly Val Val Glu Tyr Arg Val Lys Trp Lys Gly Trp Asn Gln
 20 25 30
Arg Tyr Asn Thr Trp Glu Pro Glu Asn Asn Ile Leu Asp Arg Arg Leu
 35 40 45
Ile Asp Ile Tyr
 50

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Val Gly Glu Gln Val Phe Ala Ala Glu Cys Ile Leu Ser Lys Arg Leu
1 5 10 15
Arg Lys Gly Lys Leu Glu Tyr Leu Val Lys Trp Arg Gly Trp Ser Ser
 20 25 30
Lys His Asn Ser Trp Glu Pro Glu Glu Asn Ile Leu Asp Pro Arg Leu
 35 40 45
Leu Leu Ala Phe
 50

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AGATATTCTG GATCTGATAG TGATTCAATC TCGGAAAGGA AACGGCCGAA GAAACGTGGG 60
CGACCCCGCA CTATCCCTCG GGAGAATATT AAAGGATTTA GTGATGCGGA G 111

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

AGATATTCTG GATCTGATAG TGACTCCATC ACAGAAAGAA AACGGCCAAA AAAGCGTGGA 60

AGACCTCGAA CCATTCTCG AGAAAATATT AAAGGATTTA GTGATGCAGA G 111

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTCCATCTCG GAAAGGAAAC GGCCAAAAAA GCGTGGAAGA CCACGAACTA TTCCTCGAGA 60

AAATATA 67

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AGATATTCTG GATCTGATAG TGATTCCATC TCAGAAAGAA AACGACCAAA AAAACGTGGA 60
CGACCACGAA CTATTCCCCG TGAAAACATT AAAGGATTTA GTGATGCAGA G 111

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CTCCATCTCA GAAAGAAAAC GACCAAGAAA ACGTGGACGA CCACGAACTA TTCCTCGTGA 60
AAATATT 67

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GATCTGATAG TGA TCCATC TCAGAAAGAA AACGACCAAG AAAACGTGGA CGACCACGAA 60
CTATCCCTCG GGAGAATATT AAAGGATTTA GCGATGCAGA GATTAGGCGG T 111

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ATATTCTGGA TCTGATAGTG AYTC

24

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

AGATATTCCG GATCTGATAG TGA

23

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

TTTCCTAAAT CGCTACGTCT

20